



#5

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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 65 70 75
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gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050
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tatgaaattg gccgatttca agaacacatc tccttttcaa cccattcct 1150
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gccattcaa aatgatcttt accgtggcct gcccattgct tatggtcccc 1400
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<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
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<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315

Pro Lys Ala Val

<210> 11

<211> 2720

<212> DNA

<213> Homo sapiens

<400> 11

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gccccttggg ccgtcgccac cactgtagtc atgtacccac cgccgccgcc 150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300
gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
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gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450
caccgacctt gagaacttac ctgagatttc gtcacagaag acacaaagac 500
acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
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ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650
gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
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aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100
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 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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	20	25	30
Val Ala Thr Thr	Val Val Met Tyr Pro	Pro Pro Pro Pro Pro	Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr Leu	Ser Phe Gly Glu Ser Tyr	
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg Arg	Ser Cys Trp Arg Lys Trp	
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg Asn	Met Ile Leu Phe Leu Leu	
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu Leu	Phe Tyr Ile Asn Leu Ala	
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	

290					295					300				
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser
				305					310					315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu
				320					325					330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu
				335					340					345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn
				350					355					360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser
				365					370					375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr
				380					385					390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe
				395					400					405
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val

	575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro	Glu Thr
	590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys
	605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe
	620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln
	635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe
	650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp
	665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala
	680	685	690
His Pro Leu Pro	Ile Trp Thr Pro Ala		
	695		

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 13
 cgccagaagg gcgtgattga cgtc 24

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 14
 ccataccttct tcccagacag gccg 24

<210> 15
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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gcgagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
cccaccgcct ggcagtgcct gtgcccttcc gcgaacgctt cgaggagctc 400
ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtgggc ttcctggaga gcagcaacag cacggactac 550
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<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
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 1 5 10 15

 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30

 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala			50	55	60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys			65	70	75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp			80	85	90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe			95	100	105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser			110	115	120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp			125	130	135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu			140	145	150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp			155	160	165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala			170	175	180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His			185	190	195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His			200	205	210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly			215	220	225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu			230	235	240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe			245	250	255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg			260	265	270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly			275	280	285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu			290	295	300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp			305	310	315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser						320	325	

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gcgaacgctt cgaggagtcc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18
<223> Growth factor and cytokines receptors family.

<400> 22
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20 25 30
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50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23
<211> 2883
<212> DNA
<213> Homo sapiens

<400> 23
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ggctccgggg cgcccgtgta ggccagtgcg ccgccgctcg cccgcagggc 200
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<212> PRT
<213> Homo sapiens

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<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

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Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	
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Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
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Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
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Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	
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				245					250					255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
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Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
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Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln	305	310	315
Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg	320	325	330
Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser	335	340	345
Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp	350	355	360
Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln	365	370	375
Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro	380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe	395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val	410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr	425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu	440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu	455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys	470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu	485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala	500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg	515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile	530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met	545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly	560	565	570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys
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Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr
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Ser

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

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<211> 24

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<223> Synthetic oligonucleotide probe

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<210> 27

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgaaggag ttatcagaga cattgagagg caaattcgga 150

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 <212> PRT
 <213> Homo sapiens

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 <223> Signal peptide.

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 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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 Lys Gly Ser Gln Lys Ser
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 <212> DNA
 <213> Homo sapiens

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<211> 322
<212> PRT
<213> Homo sapiens

<400> 31
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35 40 45
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	110	115	120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	125	130	135
His Ala Ile Ala	Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	290	295	300
Ala Ile Asn Leu	Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala	305	310	315
His Leu Val Phe	Val Lys Val	320		

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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 ccccgcccca gccaggggtgt taatgccac gtagtggagg cctctggcag 3450
 atcctgcatt ccaaggtcac tggactgtac gtttttatgg ttgtgggaag 3500
 ggtgggtggc tttagaatta agggccttgt aggccttggc aggtaagagg 3550
 gccaaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600
 ggctcattag gtgtttatct tgttctatct aagaatttgt tttattaaat 3650
 taatataaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgtcctttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
ctggatgcta atgtgtccag taaatgatcc cttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
ttccactcaa tgagtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggy cgctctgtta cacaagcaag atacagccag cccaccta 50
ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100
ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
caatctattc ttgccacatc aagggtattgt tattccttta aaaaaaacc 300
aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
atataaccac ctcaaattctc aaggcgagtc attccccctcc tttgaatcta 550
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
gatgaagatc ttttgcccat ctacgacat cccaatgcta cacctgctct 750
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
ccatctgtga ccccttgat agtggaacca agtggtatggc ttaccacaaa 900
cagtgatagc ttactgggt ttaccctta tcaagaaaaa acaactctac 950
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050
aggtgctatt ctgggtgtct cattgcttac tcttgtgggc tacttgttgt 1100
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gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250
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gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400
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aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650
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catagcccag agttttctgtt attgggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctacca ggaaagtaat agcttcttta aaagtcttca 2000
aaggttttgg gaattttaac ttgtottaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105

Ile Ser Thr Ser	Pro Pro Leu Ile His Ser Phe Val Ser Lys Val	110	115	120
Pro Trp Asn Ala	Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser	125	130	135
Ala His Pro Asn	Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr	140	145	150
Trp Ser Leu Val	Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser	155	160	165
Ile Thr Val Ser	Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val	170	175	180
Thr Pro Leu Ile	Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser	185	190	195
Asp Ser Phe Thr	Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu	200	205	210
Gln Pro Thr Leu	Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn	215	220	225
Thr Ser Asp Pro	Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe	230	235	240
Gly Ala Ile Leu	Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu	245	250	255
Val Gly Tyr Leu	Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser	260	265	270
His Arg Arg Leu	Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu	275	280	285
Asp Asn Ala Pro	Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser	290	295	300
Tyr Tyr Asn Pro	Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu	305	310	315
Glu Asn Ala Arg	Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu	320	325	330
Arg Thr Ser Val				

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100
cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
tacaagtact tcatgccccaa gagcaccatt taccgtggag agatgtgctt 350
ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
atcattgatg tgccctgtccc cagtttctct gatagtgacc ctgcagcaat 500
tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550
ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600
aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagtgc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatcttt attaccaac ttgcaataa cagaaagtcc 750
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tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgactttaa cattaagggt tatgggatac 950
tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000
gaaaaaaaaa aaaactacta accactgcaa gctcttgta aatttttagtt 1050
taattggcat tgcttgtttt ttgaaactga aattacatga gtttcatttt 1100
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
tttaaaattt gaaatatatt aaattgtttt tgaacttttt gtgtaaaata 1300
tatcagatct caacattggt ggtttctttt gtttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
aatgcagtga ttcttttctca ctactatctg tattgtggaa tgcacaaaat 1500

tgtgtaggtg ctgaatgctg taaggagttt aggttgatg aattctacaa 1550

ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50						55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

	230		235		240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile					
	245		250		255
Val Glu Thr Lys Ile Cys Gln Glu					
	260				

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 45
 gggaactgct atctgatgcc 20

<210> 46
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 caggatctcc tcttgacgac tgcagc 26

<210> 47
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 47
 cttctcgaac cacataagtt tgaggcag 28

<210> 48
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50
cacggactct ctcttcacgc ccaggtgccc cccactctcg ctccattcgg 100
cgggagcacc cagtctgta cgccaaggaa ctggtcctgg gggcaccatg 150
gtttcggcgg cagccccag cctcctcacc cttctgttgc tgctgctggg 200
gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
ccgagcctcc cgccaccctg gaccccggcc ctccagccca catcgatggg 350
gccccagccc acaaccctgg ggggcccacc acccccacc aacttctcgg 400
atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
ggctccctgg cctttctgct gatgttcacc gtctgtgccg cggtcaccac 500
ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550
agaagtacgt ggaccagagt gaccgggccg ggggcccccg ggccttcagt 600
gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
ccccaccag ggctgcactg ggcgggtggg acggagccag gatggtggag 750
ggcaggggag cagaggaaga ggagaagggc agccaggagg gggaccagga 800
agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850
cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000
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cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150

cagaaatgct ggtccccggt gccccggagg aatcttacca agtgccatca 1200
 tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
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 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgctc ttaattttcc tgaaggtggc cccctgtttc tagttgttcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500
 caagcacccc cggcctgggg gtgagtttct catcccgtca ctgctgctgg 1550
 gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
 ggggctgggg aagggttttct gacgcccagc ctggagcagg ggggccctgg 1700
 ccacccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
 gtcagtcctc gacagggagc ctgggctccg tctgtcttta gggaggctct 1800
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

80					85					90				
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala
				95					100					105
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln
				110					115					120
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys
				125					130					135
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe
				140					145					150
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala
				155					160					165
Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
				170					175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
				260					265					270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
				275					280					

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250

ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400
aagggaccag agaagcagtt ggactggag tcaggcaggt tccaggcttt 450
ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
gggaaacact gggcagcaga ttggcagaca ggcagaagat gtcattcgac 550
acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700
tccacggata ccccgaaac tcagcaggca gctttggaat gaatcctcag 750
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caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
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cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
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<212> PRT

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Arg Gly Asp Ser	Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310	315
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Glu Ser Gly Ile	Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn	350	355	360
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Gly Asp Asn Tyr	Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val	Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe	Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
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Ser Ser Arg Ile	Pro	440		

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gggacaagta ctggcactcc atcagccacc tgcagccaga gacctcctac 2700
gacattaaga tgcagtgtt caatgaagga ggggagagcg agttcagcaa 2750
cgtgatgatc tgtgagacca aagctcggaa gtcttctggc cagcctggtc 2800
gactgccacc cccaactctg gccccaccac agccgcccct tcctgaaacc 2850
atagagcggc cgggtgggcac tggggccatg gtggctcgct ccagcgacct 2900
gccctatctg attgtcgggg tcgtcctggg ctccatcggt ctcacatcg 2950
tcaccttcat ccccttctgc ttgtggaggg cctggtctaa gcaaaaacat 3000
acaacagacc tgggttttcc tcgaagtgcc ctccaccct cctgcccgtg 3050
tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100
cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150
aataggggct gcccctcggc tgcagtgggc taccgggca tgaagcccca 3200
gcagcactgc ccaggcgagc ttcagcagca gagtgcacc agcagcctgc 3250
tgaggcagac ccattctggc aatggatatg acccccaaag tcaccagatc 3300
acgaggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350
gcccagcagc tccactcacc agctgctgca gcccatac gactgctgcc 3400
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 gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700
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 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
 agataagctg gcaagaggaa ggatcccagg cacatgggtc atcacgagca 4050
 tgagggaaca gcaaggggca cggtatcaca gcctggagac acccacacag 4100
 atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
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 aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu
 1 5 10 15
 Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
 20 25 30
 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
 35 40 45
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
 50 55 60
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
 65 70 75
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
 80 85 90

Leu Val Ile Thr	Ala Leu Asn Asn His	Thr Val Gly Arg Tyr	Gln
	95	100	105
Cys Val Ala Arg	Met Pro Ala Gly Ala	Val Ala Ser Val Pro	Ala
	110	115	120
Thr Val Thr Leu	Ala Asn Leu Gln Asp	Phe Lys Leu Asp Val	Gln
	125	130	135
His Val Ile Glu	Val Asp Glu Gly Asn	Thr Ala Val Ile Ala	Cys
	140	145	150
His Leu Pro Glu	Ser His Pro Lys Ala	Gln Val Arg Tyr Ser	Val
	155	160	165
Lys Gln Glu Trp	Leu Glu Ala Ser Arg	Gly Asn Tyr Leu Ile	Met
	170	175	180
Pro Ser Gly Asn	Leu Gln Ile Val Asn	Ala Ser Gln Glu Asp	Glu
	185	190	195
Gly Met Tyr Lys	Cys Ala Ala Tyr Asn	Pro Val Thr Gln Glu	Val
	200	205	210
Lys Thr Ser Gly	Ser Ser Asp Arg Leu	Arg Val Arg Arg Ser	Thr
	215	220	225
Ala Glu Ala Ala	Arg Ile Ile Tyr Pro	Pro Glu Ala Gln Thr	Ile
	230	235	240
Ile Val Thr Lys	Gly Gln Ser Leu Ile	Leu Glu Cys Val Ala	Ser
	245	250	255
Gly Ile Pro Pro	Pro Arg Val Thr Trp	Ala Lys Asp Gly Ser	Ser
	260	265	270
Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly		665	670	675
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu		680	685	690
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr		695	700	705
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr		710	715	720
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met		725	730	735
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr		740	745	750
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys		755	760	765
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His		770	775	780
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn		785	790	795
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr		800	805	810
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro		815	820	825
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg		830	835	840
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro		845	850	855
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
950 955 960

Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
965 970 975

Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
980 985 990

Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
995 1000 1005

Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
1010 1015 1020

Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
1025 1030 1035

Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
1040 1045 1050

Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
1055 1060 1065

Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
1070 1075 1080

Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
1085 1090 1095

Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
1100 1105 1110

Pro Pro Leu Thr Ile
1115

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgaggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccatt 50
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100
cacgggcccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcgtc 150
tgctgtctcct gctactgtcg ctgctgtgc ggcagcccgt aaccgcgcgcg 200
gagaccacgc cgggcgcgcc cagagccctc tccacgctgg gctccccag 250
cctcttcacc acgccgggtg tcccagcgc cctcactacc ccaggcctca 300
ctacgccagg caccccc aaa accctggacc ttcggggctg cgcgcaggcc 350
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
cagcctctct gtgctgcga gtttctatgt gctgggggtg cgctacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
 catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatggtga 1050
 cactgtccat gggggtgctg cagtgaacc tgcttgctaa cgtgtccact 1100
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
 cgggattggt ggaaattatg acgggactgg ccggttccct caggggctgg 1200
 aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400
 ctogtgctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
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 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgctgacaca gtcgggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
 1 5 10 15
 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro			
				65					70					75			
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser			
				80					85					90			
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg			
				95					100					105			
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe			
				110					115					120			
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val			
				125					130					135			
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp			
				140					145					150			
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His			
				155					160					165			
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala			
				170					175					180			
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val			
				185					190					195			
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser			
				200					205					210			
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys			
				215					220					225			
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met			
				230					235					240			
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val			
				245					250					255			
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala			
				260					265					270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro			
				275					280					285			
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu			
				290					295					300			
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly			
				305					310					315			
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu			
				320					325					330			
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg			
				335					340					345			

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
	350	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
	365	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
	380	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
	395	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
	410	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
	425	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
	440	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
	455	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
	470	480
Thr Phe Thr Gln Trp Leu Cys		
	485	

<210> 64

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
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atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaagggtgc 600
ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650
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ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850
aagagggatg tggctctctga tctctgttgt cttcttgggt ctttgggggt 900
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
ctcaggagtg gatgcgatct gtctctctctg gctccactct tgccgccttc 1000
cagctctgag tcttggaat gttgttacct ttggaagata aagctgggtc 1050
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gttcctttct gcagtgggtc ttatcaccac ctccctccca gcccggcgc 1150

ctcagcccca gccccagctc cagccctgag gacagctctg atgggagagc 1200
 tgggccccct gagcccaactg ggtcttcagg gtgcactgga agctggtgtt 1250
 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300
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 gcctcttgct cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tcctcttgct ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 155 160 165

Met Leu Ser

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<400> 69
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
agttcatagg gtcttggttc cccgaaccag gaagggttga gggaacacaa 100
tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggctctccc 150
tccctttgca ttcccacccc tccgggcttt gcgtcttctt ggggaccccc 200
tcgcccggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
tcgccggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
gcatgtgctg ccccgatacc cgctgcaata atggcatctg tatcccagtt 600
actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650
cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45
Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly
				50					55					60
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala
				65					70					75
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys
				80					85					90
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg
				95					100					105
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr
				110					115					120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu	125	130	135
Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg	140	145	150
Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu	155	160	165
Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly	170	175	180
Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys	185	190	195
Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln	200	205	210
Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu	215	220	225
Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	230	235	240
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val	245	250	255
Cys Gln Lys Ile			

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

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<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

275										280					285				
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln					
				290					295					300					
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn					
				305					310					315					
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr					
				320					325					330					
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg					
				335					340					345					
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp					
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<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 73
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<210> 74
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 74
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<210> 75
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 75
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<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 76

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 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75
Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
				80					85					90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
				95					100					105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
				110					115					120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
				125					130					135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys	395	400	405
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser	410	415	420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
425 430 435

Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
440 445 450

Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
455 460 465

Ala Cys Ser Thr Leu Leu Val His Leu Ile
470 475

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

ttttgcggtc accattgtct gc 22

<210> 81

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 81

cgtaggtgac acagaagccc agg 23

<210> 82

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82

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<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
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cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
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<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu	1	5	10	15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln	20	25	30	
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu	35	40	45	
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln	50	55	60	
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala	65	70	75	
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala	80	85	90	
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn	95	100	105	
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser	110	115	120	
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu	125	130	135	
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His	140	145	150	
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys	155	160	165	
Leu	Gly	Tyr	Ala	Leu	Arg	Pro	Gln	Glu	Lys	Gly	His	Ser	Pro	Glu	170	175	180	
Asp	Ile	Tyr	Gln	Met	Ala	Leu	Asn	Gln	Ala	Leu	Lys	Asp	Leu	Lys	185	190	195	

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu	455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly	470	475	480

Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys
485 490 495

Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro
500 505 510

Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu
515 520 525

Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp
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Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu
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Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His
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<210> 85

<211> 3316

<212> DNA

<213> Homo sapiens

<400> 85

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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile		
50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys		
65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg		
80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val		
95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn		
110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu		
125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu		
140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys		
155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His		
170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala		
185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr		
200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu		
215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile		
230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu		
245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro		
260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu		
275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe		
290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys		
305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr		

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	

605	610	615
Asn Ile Tyr Asn Arg Ser Gln Pro Val	Leu Gln Ile Phe Val	His
620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val	Gly Val Val Val Pro	Asp
635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys	Gly
650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln	Val Val Arg Glu Ala	Ile
665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys	Thr
680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu	His Pro Glu Pro Phe	Ser
695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg	Gly
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Glu Leu Ser Lys Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr	Glu
725	730	735

His Ile Gln Asp

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

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cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200

ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250

caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300

atcctggaca ctgcggcagc catcagtga gccaatgaag acccagagcc 350

agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400

gaggcagtgg tccccggcgg gtctggacg tagaggtgta ttcaagtcgc 450

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<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met	Asp	Asp	Trp	Lys	Pro	Ser	Pro	Leu	Ile	Lys	Pro	Phe	Gly	Ala
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Arg	Lys	Lys	Arg	Ser	Trp	Tyr	Leu	Thr	Trp	Lys	Tyr	Lys	Leu	Thr
				20					25					30

Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu
				35					40					45

Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
				50					55					60

Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
				65					70					75

Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
				80					85					90

Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser
				95					100					105

Ser Arg Ser Lys Val Tyr Val Ala Val	Asp Gly Thr Thr Val	Leu
110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg	Gly Ile His Val Ile	Val
125	130	135
Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe	Asp
140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala	Met Val Leu Phe Leu	Asn
155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile	Cys Thr Val Lys Asp	Glu
170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala	Lys Ala Leu Leu Arg	Ser
185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu	Gly Trp Arg Asp Thr	Trp
200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro	Val Phe Gly Glu Lys	His
215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp	Gly Asp Pro Val Leu	Leu
230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala	Glu Glu Ala Glu Cys	His
245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg	Arg Arg Arg Phe Cys	Ser
260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys	Ser Cys Lys Asp Pro	Thr
275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu	Pro Asp Asn Lys Val	Leu
290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly	Asn Arg Pro Asn Tyr	Leu
305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser	Ala Gln Gly Val Ser	Pro
320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly	Tyr Tyr Glu Glu Pro	Met
335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg	Gly Ile Gln His Thr	Pro
350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser	Gln His Tyr Lys Ala	Ser
365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro	Glu Ala Lys Phe Ala	Val
380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe	395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr	410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu	425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly	440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys	455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg	470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val	485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly	500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val	515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala	530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu	545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr	560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp	575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp	590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe	605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro	620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu	635	640	645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr	650	655	660

<210> 89

<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
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<220>
<223> Synthetic oligonucleotide probe

<400> 90
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<210> 91
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

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<210> 95

<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

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Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe
				20					25					30

Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu
				35					40					45

Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His
				50					55					60

Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser
				65					70					75

Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser
				80					85					90

Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His
				95					100					105

Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu
				110					115					120

Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp
				125					130					135

Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu
				140					145					150

Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala
				155					160					165

Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val
				170					175					180

Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser
				185					190					195

Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His
				200					205					210

Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr
				215					220				225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val
				230					235				240	
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
				245					250				255	
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265				270	
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
				275					280				285	
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
				290					295				300	
Leu	Ser	Val	Gly	His	Gln	His								
				305										

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 96
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<210> 97
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
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<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
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ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met	Met	Gly	Leu	Gly	Asn	Gly	Arg	Arg	Ser	Met	Lys	Ser	Pro	Pro
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Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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230	235	240
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245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
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Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
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Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
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<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165

Gln Leu Thr Ser	Ala Gly Arg Arg Val	Val Phe Met Gly Asp Asp	170	175	180
Thr Trp Lys Asp	Leu Phe Pro Gly Ala	Phe Ser Lys Ala Phe Phe	185	190	195
Phe Pro Ser Phe	Asn Val Arg Asp Leu	Asp Thr Val Asp Asn Gly	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His Lys	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg	440	445	450

Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	455	460	465
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Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	485	490	495
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	500	505	510
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	515	520	525
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	530	535	540
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	545	550	555
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	560	565	570
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	575	580	585
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	590	595	600
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	605	610	615
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	620	625	630
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	635	640	645
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	650	655	660
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	665	670	675
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	680	685	690
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	695	700	705
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	710	715	720
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	725	730	735

Val Ser Gly Ala	Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
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Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055					1060					1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
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Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60

Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75

Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
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Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
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Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
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Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	425	430	435
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<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 105

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<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

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<210> 107

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

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 aaaaaaaaaa gaaa 1114

<210> 111
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 111
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 35 40 45
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
 50 55 60
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
 65 70 75
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
 80 85 90
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
 95 100 105
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
 110 115 120
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
 125 130 135
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
 140 145 150
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
 155 160 165
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
 170 175 180
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
 185 190 195
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

	200	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg			
	215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly			
	230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val			
	245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly			
	260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala			
	275	280	

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

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<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

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				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
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Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	
				230					235					240	
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
				245					250					255	
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
				260					265					270	
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
				275					280					285	
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
				290					295					300	
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
				305					310					315	
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	
				320					325					330	

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

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 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgccccg 150
 agcgccggct gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200
 cggtgcggg acctgactag attctacgac aaggacttt ctttgcata 250
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 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser
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Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

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<210> 120

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

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<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly				

	170	175	180
Val Pro Tyr Thr	Cys Cys Ile Arg Asn	Thr Thr Glu Val Val	Asn
	185	190	195
Thr Met Cys Gly	Tyr Lys Thr Ile Asp	Lys Glu Arg Phe Ser	Val
	200	205	210
Gln Asp Val Ile	Tyr Val Arg Gly Cys	Thr Asn Ala Val Ile	Ile
	215	220	225
Trp Phe Met Asp	Asn Tyr Thr Ile Met	Ala Cys Ile Leu Leu	Gly
	230	235	240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu	Tyr
	245	250	255
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr	Asp
	260	265	270
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala	Gly
	275	280	285
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 124
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<210> 125
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
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<210> 126
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 126

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<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu				

170										175					180				
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu					
				185					190					195					
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly					
				200					205					210					
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu					
				215					220					225					
Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys					
				230					235					240					
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser					
				245					250					255					
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu					
				260					265					270					
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser					
				275					280					285					
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu					
				290					295					300					
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His					
				305					310					315					
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp					
				320					325					330					
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr					
				335					340					345					
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu					
				350					355					360					
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu					
				365					370					375					
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr					
				380					385					390					
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp					
				395					400					405					
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp					
				410					415					420					
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu					
				425					430					435					
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu					
				440					445					450					
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys					

	455		460		465									
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser
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Pro Val Ser Gln

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 <211> 2213
 <212> DNA
 <213> Homo sapiens

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<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

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Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys	50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile	65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys	80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg	95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp	110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser	125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg	140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln	155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val	170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu	185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met	200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys	215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg	230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn	245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His	260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu	275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys	290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser			

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Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr			
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Ser Phe Leu Met Ser			
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<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
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<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132

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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25						30
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40						45
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55						60
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70						75
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85						90
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100						105
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115						120
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130						135
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145						150
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
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Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175						180
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190						195
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205						210
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220						225
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235						240
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250						255

Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr	Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr	Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met	Leu Gly Glu Ile Ile	Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln	Lys Thr Ile Val Ile	Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met	Glu His Arg Gln Phe	Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala	His Val Pro Leu Leu	Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu	Gln Val Ser Asn Val	Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly	Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

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Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	35	40	45	
Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	50	55	60	
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	65	70	75	
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	80	85	90	
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	95	100	105	
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	110	115	120	
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro	125	130	135	
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro	140	145	150	
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	170	175	180	
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	185	190	195	
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	200	205	210	

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Leu Thr Gly Tyr Val
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 <211> 610
 <212> DNA
 <213> Homo sapiens

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 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	65		70		75
Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe					
	80		85		90
Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser					
	95		100		105
Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro					
	110		115		

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

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<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
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				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275		280		285
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<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

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				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
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Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	
				290					295					300	
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	
				305					310					315	
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	
				320					325					330	
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	
				335					340					345	
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	
				350					355					360	
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	
				365					370					375	
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	
				380					385					390	
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	
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Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
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Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90

Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
			20					25						30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35					40						45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala					
				65					70					75					
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu					
				80					85					90					
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro					
				95					100					105					
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys					
				110					115					120					
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys					
				125					130					135					
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg					
				140					145					150					
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln					
				155					160					165					
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala					
				170					175					180					
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala					
				185					190					195					
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr					
				200					205					210					
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro					
				215					220					225					
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln					
				230					235					240					
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser					
				245					250					255					
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala					
				260					265					270					
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala					
				275					280					285					
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys					
				290					295					300					
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro					
				305					310					315					
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr					
				320					325					330					
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile					

	335		340		345
Gln Cys Ser Phe Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg Ala				
	350		355		360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser Leu				
	365		370		375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp Gly				
	380		385		390
Tyr Gln Ile Val Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu Glu				
	395		400		405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
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aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

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Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys	35	40	45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe	50	55	60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe	65	70	75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp	80	85	90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr	95	100	105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser	110	115	120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly	125	130	135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile	140	145	150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg	170	175	180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu	185	190	195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His	200	205	210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp	215	220	225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu	230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys	245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys			

290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
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<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 151
gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180
Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195
Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210
Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225
Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cagtcacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 156
aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
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ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
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 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
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 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Phe	Leu	Ala	Leu	Val	Ser	Val	1	5	10	15
Pro	Arg	Ala	Gln	Ala	Val	Trp	Leu	Gly	Arg	Leu	Asp	Pro	Glu	Gln	20	25	30	
Leu	Leu	Gly	Pro	Trp	Tyr	Val	Leu	Ala	Val	Ala	Ser	Arg	Glu	Lys	35	40	45	
Gly	Phe	Ala	Met	Glu	Lys	Asp	Met	Lys	Asn	Val	Val	Gly	Val	Val	50	55	60	
Val	Thr	Leu	Thr	Pro	Glu	Asn	Asn	Leu	Arg	Thr	Leu	Ser	Ser	Gln	65	70	75	
His	Gly	Leu	Gly	Gly	Cys	Asp	Gln	Ser	Val	Met	Asp	Leu	Ile	Lys	80	85	90	
Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu	95	100	105	
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile	110	115	120	
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu	125	130	135	
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu	140	145	150	
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln	155	160				

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg cccctgctct gggggagggg gagggcgga ggacagacaa 100
gtaaactgct gacgatgcag agtcccgta cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccatcccc tcgcatggct ggatttacc 200
tggtccagta gttcatggct actggttcgg ggaagggggc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacacccct atgatctcct ggatagggac ctccgtgtcc 600
ccccctggacc cctccaccac ccgctcctcg gtgctcacc tcacccaca 650
gccccaggac catggcacca gcctcacctg tcagggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950
ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtgact cagggggtgg tcgggggagc 1100
tggtgcccaca gccctggtct tcctgtcctt ctgctcatc ttggtttag 1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgccccg ctccctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttccaga tgggtgaagcc ttgggactcg cggggacagg aggccactga 1400
 caccgagtagc tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	
1				5					10					15	
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	
				20					25					30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	
				35					40					45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	
				50					55					60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	
				65					70					75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	
				80					85					90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	
				95					100					105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	
				110					115					120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	
				125					130					135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	
				140					145					150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	
				155					160					165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	
				170					175					180	

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg	Ser
	185	190	195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr	Ser
	200	205	210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr	Asn
	215	220	225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu	Thr
	230	235	240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu	Gly
	245	250	255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg	Leu
	260	265	270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg	Leu
	275	280	285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro	Ser
	290	295	300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp	Ala
	305	310	315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln	Gln
	320	325	330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly	Val
	335	340	345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val	Phe
	350	355	360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg	Lys
	365	370	375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile	Glu
	380	385	390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu	Thr
	395	400	405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro	Ala
	410	415	420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala	Ser
	425	430	435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln	Glu
	440	445	450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg	
	455	460	

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgccttcac 100
cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250
gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500
tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550
acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctaccc tccagccatg acccttcct 650
gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
20 25 30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
35 40 45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
50 55 60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
65 70 75

Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	
				80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	
				95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	
				110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	
				125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	
				140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	
				155					160					165	
Cys	Val	Pro	Glu	His											
				170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 165
 gtcctccgga aagtccttat c 21

<210> 166
 <211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggaacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccctggagga ggaggatata acagggaacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gttccgcaga tgcagagggt gaggtggctg cgggactgga agtcatcggg 50
cagagggtctc acagcagcca aggaacctgg ggcccgtctc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtggg 250
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag cactgagtc cttccccac cccggcttca 400
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500

ctcacgtgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800
ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcacctc catttccact 900
tggtgtttgg ttctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15
Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
20 25 30
His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
35 40 45
Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
50 55 60
Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
65 70 75
Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
80 85 90
Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
95 100 105

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcggga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
cgtgtagaca ccaggctttc gggcg 25

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctggc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150
agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
tgtgaccaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750
agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcatcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 187

gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaacaaaa acttcctgtg ctaagtgcc 100

cccaaagtct tcctgtgtca ataactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200

aagccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

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ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
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<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
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gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggctg aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acagggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
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 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
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<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg
				20					25					30
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu
				35					40					45
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala
				50					55					60
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His
				65					70					75
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly
				80					85					90
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His
				95					100					105
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val
				110					115					120

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	
				125					130					135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	
				140					145					150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	
				155					160					165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	
				170					175					180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	
				185					190					195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	
				200					205					210	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	
				215					220					225	
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	
				230					235					240	
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn								
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 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
 tcagtgaac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600

ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
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<210> 196

<211> 150

<212> PRT

<213> Homo' sapiens

<400> 196

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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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ggggtcggcg ccgcctgctg cgccgcctg gcgctggcct tggcgctggc 150

gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200

gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250

cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300

caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350

tgcattctgga agacaaccag gtcagcgtca tcgagagagg cgccttcag 400

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ccttcagaaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500

tgagtgaata ccagatccag gggatcccg ggaaggcgtt ccgcggcatc 550

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atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750

ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800

cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg 850

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
				20				25					30	

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

35					40					45				
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
				50					55					60
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
				65					70					75
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
				80					85					90
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95					100					105
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110					115					120
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
				125					130					135
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140					145					150
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155					160					165
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu
				170					175					180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg
				185					190					195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu
				200					205					210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp
				215					220					225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr
				230					235					240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp
				245					250					255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro
				260					265					270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr
				275					280					285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu
				290					295					300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu
				305					310					315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr

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Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser		Lys	Asn	Gln	Ile	Ser	Asp				
				335										340					345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu		Lys	Ser	Leu	Thr	Ser	Leu				
				350										355					360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu		Ile	Ala	Lys	Gly	Leu	Phe				
				365										370					375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu		Leu	Leu	Asn	Ala	Asn	Lys				
				380										385					390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe		Gln	Asp	Leu	Gln	Asn	Leu				
				395										400					405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys		Leu	Gln	Thr	Ile	Ser	Lys				
				410										415					420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile		Gln	Thr	Leu	His	Leu	Ala				
				425										430					435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His		Leu	Lys	Trp	Leu	Ala	Asp				
				440										445					450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr		Ser	Gly	Ala	Arg	Cys	Ser				
				455										460					465
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg		Ile	Ser	Gln	Ile	Lys	Ser				
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Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu		Asp	Tyr	Arg	Ser	Arg	Phe				
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Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val		Cys	Pro	Glu	Lys	Cys	Arg				
				500										505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser		Asn	Gln	Lys	Leu	Val	Arg				
				515										520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val		Thr	Asp	Leu	Arg	Leu	Asn				
				530										535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala		Thr	Gly	Ile	Phe	Lys	Lys				
				545										550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu		Ser	Asn	Asn	Lys	Ile	Lys				
				560										565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly		Ala	Ala	Ser	Val	Gln	Glu				
				575										580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu		Thr	Val	His	Gly	Arg	Val				
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Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr		Leu	Met	Leu	Arg	Ser	Asn				

605										610					615				
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser					
				620					625					630					
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr					
				635					640					645					
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu					
				650					655					660					
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly					
				665					670					675					
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys					
				680					685					690					
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala					
				695					700					705					
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln					
				710					715					720					
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val					
				725					730					735					
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met					
				740					745					750					
Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr					
				755					760					765					
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile					
				770					775					780					
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe					
				785					790					795					
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg					
				800					805					810					
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu					
				815					820					825					
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu					
				830					835					840					
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly					
				845					850					855					
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu					
				860					865					870					
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser					
				875					880					885					
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr					

890										895					900				
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala					
				905					910					915					
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr					
				920					925					930					
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr					
				935					940					945					
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile					
				950					955					960					
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser					
				965					970					975					
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly					
				980					985					990					
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys					
				995					1000					1005					
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys					
				1010					1015					1020					
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile					
				1025					1030					1035					
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys					
				1040					1045					1050					
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly					
				1055					1060					1065					
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala					
				1070					1075					1080					
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly					
				1085					1090					1095					
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu					
				1100					1105					1110					
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln					
				1115					1120					1125					
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu					
				1130					1135					1140					
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu					
				1145					1150					1155					
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu					
				1160					1165					1170					
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln					

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser 1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp 1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly 1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu 1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn 1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser 1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly 1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg 1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 200

ttgttgcat tgaggaggag cagc 24

<210> 201

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 201

gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202

<211> 753

<212> DNA

<213> Homo sapiens

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gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
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 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
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 gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
gcaggctttg aggatgaagg ctgc 24

<210> 205
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 205
ctcattggct gcctgggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 207
tcagtgaacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

ctacactcgt tgcaaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250
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gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
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<210> 210
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 210
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 20 25 30
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 35 40 45
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
 50 55 60
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
 65 70 75
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
 80 85 90
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
 95 100 105
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
 110 115 120
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
 125 130 135
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
 140 145 150
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

	155	160	165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu	Arg
	170	175	180
Val Leu Glu Asn	Val Glu His Tyr Gln	Glu Leu Lys Lys Met	Val
	185	190	195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser	Phe
	200	205	210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys	Val
	215	220	225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu	Glu
	230	235	240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly	Gly
	245	250	255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys	Glu
	260	265	270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile	Arg
	275	280	285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala	Arg
	290	295	300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu	Tyr
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Arg Tyr Val Thr	Lys Leu Leu Val		
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<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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ccttctggtt tggcaggcgc ctcgtgggta gtttgggcac tggtgatgta 300
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 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala	20	25	30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu	35	40	45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn	50	55	60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg	65	70	75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His	80	85	90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys	95	100	105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn	110	115	120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu	125	130	135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu	140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser	155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val	170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln	185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu	200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu	215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser	245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser	260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys	275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys	290	295	300

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
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Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320					325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335					340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350					355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365					370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380					385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395					400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410					415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425					430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440					445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455					460						

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgctct ctgtcacctt gggcctcttt gcagtggagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggtt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaaata 700
 tgtttttagt taacattaag acttatatac agttttaggg gacaattaa 750
 aaaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
 tcccggaccc tgccgccctg ccactatgtc ccgccgctct atgctgcttg 50

cctgggctct cccagcctc ctctgactcg gagcggctca ggagacagaa 100
gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcggggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT
<213> Homo sapiens

<400> 216
Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
1 5 10 15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217
 <211> 1871
 <212> DNA
 <213> Homo sapiens

<400> 217
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 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
 tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150
 cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcgaa 200
 gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac aggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
 ctcccgagac cagctcaga gctcagccac ctggagctgc tcccagccct 700
 tcaaagtcgt ctgtgtctac atcgccttct acagcacgga ctatcggctg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccgggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900
 gttgggcctc aggcagggag gggggtggag acgaggagat gccaagtggg 950
 gccagggcca agtctcaagt ggcagagaaa ggggcccaag tgctgggtccc 1000
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcattgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
 gcaacagggg gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
 atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtggg 1300
 gccagaggag ctctccagcc ctgcctagtg ggcgcctga gccccttgtc 1350
 gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
 ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500
 cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550
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 tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
 aaccgtgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
 aataaagctt gcccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1					5				10					15

Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	215	220	225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	230	235	240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				245	250	

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gcaggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100

gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200

gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250
tcttccccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
agcgccagcc ggctgcggtc gccacacgg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400
ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctgaacccg gccacggact ccaagggctc 500
ctcttctccc ccgctgggga tatcggtccg ggcgccaac tccaaggtcg 550
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
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tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
tgttactcgt gaagctgcc acaatggtgt cctgctctac ctagataaag 850
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cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
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gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgcaa 1350
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
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aactggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

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 cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750
 aatgattgat aataaccact ttattaaaaa cctaagggtt ttttttttc 1800
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950
 ttcaaataat ccataatctaa atttagtgc atatcttgct ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu	1	5	10	15
Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp	20	25	30	
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp	35	40	45	
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu	50	55	60	
Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	65	70	75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	80	85	90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	95	100	105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	110	115	120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	125	130	135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	140	145	150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	155	160	165	

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
185 190 195

Phe Leu Val Phe Pro Leu
200

<210> 221
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 221
acggctcacc atgggctccg 20

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
aggaagagga gcccttgagg tccg 24

<210> 223
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
 tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
 gtgaagggtt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400
 ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
 ttcattggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
 gtcattatct tgctgcatgt attctggggc attgtatatt ttgatggctg 550
 tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
 tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
 tcagcattta taatcctggg gctcatgggc acctgggcat tcttagctgc 700
 gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
 actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
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 tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
 ta 902

<210> 225

<211> 257

<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	1	5	10	15
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	20	25	30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	50	55	60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	95	100	105	

Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

<210> 226

<211> 3939

<212> DNA

<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200

tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250

gtctgtgaac gtcctgaaca agcagaaggg ggccgcttg ctgtttgtgg 300

tccgccagaa ggaggctgtg gtgtccttcc aggtgccct aatcctgcga 350

gggatgtttc agcgcaagta cctctaccaa aaagtgaac gaaccctgtg 400

tcagccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450

tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550
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gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350
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<210> 227
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 227
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 Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
 20 25 30
 Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser

	125	130	135
Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg	140	145	150
Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn	155	160	165
Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu	170	175	180
Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe	185	190	195
Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr	200	205	210
Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met	215	220	225
Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser	230	235	240
Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala	245	250	255
Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro	260	265	270
Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser	275	280	285
Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys	290	295	300
Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala	305	310	315
Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala	320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys			

	410	415	420
Asn Val Ile Arg	Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu	Ala
	425	430	435
Arg Lys Asp Lys	Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr	Phe
	440	445	450
Trp Asn Ile Ala	Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val	Val
	455	460	465
Gln Leu Val Ile	Thr Tyr Gln Thr Val	Val Asn Val Thr Gly	Asn
	470	475	480
Gln Asp Ile Cys	Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu	Gly
	485	490	495
Asn Leu Ser Ala	Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr	Ile
	500	505	510
Leu Leu Gly Leu	Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu	Ile
	515	520	525
Asn His Asn Arg	Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu	Glu
	530	535	540
Cys Gly Ile Pro	Lys His Phe Gly Leu	Phe Tyr Ala Met Gly	Thr
	545	550	555
Ala Leu Met Met	Glu Gly Leu Leu Ser	Ala Cys Tyr His Val	Cys
	560	565	570
Pro Asn Tyr Thr	Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr	Met
	575	580	585
Ile Ala Gly Leu	Cys Met Leu Lys Leu	Tyr Gln Lys Arg His	Pro
	590	595	600
Asp Ile Asn Ala	Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala	Ile
	605	610	615
Val Ile Phe Phe	Ser Val Leu Gly Val	Val Phe Gly Lys Gly	Asn
	620	625	630
Thr Ala Phe Trp	Ile Val Phe Ser Ile	Ile His Ile Ile Ala	Thr
	635	640	645
Leu Leu Leu Ser	Thr Gln Leu Tyr Tyr	Met Gly Arg Trp Lys	Leu
	650	655	660
Asp Ser Gly Ile	Phe Arg Arg Ile Leu	His Val Leu Tyr Thr	Asp
	665	670	675
Cys Ile Arg Gln	Cys Ser Gly Pro Leu	Tyr Val Asp Arg Met	Val
	680	685	690
Leu Leu Val Met	Gly Asn Val Ile Asn	Trp Ser Leu Ala Ala	Tyr

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Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala					
				710					715					720					
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile					
				725					730					735					
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu					
				740					745					750					
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe					
				755					760					765					
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser					
				770					775					780					
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp					
				785					790					795					
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser					
				800					805					810					
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln					
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Arg	Asp	Lys	Ile	Tyr	Val	Phe													
				830															

<210> 228
 <211> 2848
 <212> DNA
 <213> Homo sapiens

<400> 228
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 taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg 450
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Ala	Leu	Pro	Lys	Ala	Gln	Pro	Ala	Glu	Leu	Ser	Val	Glu	Val	Pro
				20					25					30

Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
				35					40					45

Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60

Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75

Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80										85					90				
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

365					370					375				
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
				455					460					465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
				470					475					480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
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Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly
				605					610					615
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp
				620					625					630
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
				635					640					645
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His

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Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		
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<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

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<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aaccccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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<210> 234
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234

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Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195	

Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr	Ser
200	205		210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn	Pro
215	220		225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg	Lys
230	235		240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp	Pro
245	250		255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser	Asp
260	265		270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser	Glu
275	280		285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly	Asn
290	295		300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu	Met
305	310		315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu	Glu
320	325		330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser	Val
335	340		345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val	Tyr
350	355		360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly	Ile
365	370		375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr	Gly
380	385		390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu	Thr
395	400		405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn	Leu
410	415		420

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236

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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr	20	25	30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr	35	40	45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val	50	55	60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val	65	70	75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr	80	85	90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr	95	100	105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser	110	115	120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala	125	130	135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly	140	145	150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe	155	160	165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys	170	175	180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp	185	190	195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala	200	205	210	

Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe
215		220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met
230		235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn
245		250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe
260		265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala
275		280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys
290		295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser
305		310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala
320		325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser
335		340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser
350		355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile
365		370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn
380		385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile
395		400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	
410		415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

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<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	
Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80				85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95				100					105	

Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
110		115	120
Thr Asn Ser Glu	Ser Ser Thr Pro Ser	Ser Gly Ala Ser Thr	Val
125		130	135
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ser Gly Ala Ser Thr	Ala
140		145	150
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr	Ala
155		160	165
Thr Asn Ser Glu	Ser Ser Thr Leu Ser	Ser Gly Ala Ser Thr	Ala
170		175	180
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
185		190	195
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
200		205	210
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr	Ala
215		220	225
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
230		235	240
Thr Asn Ser Glu	Ser Arg Thr Thr Ser	Asn Gly Ala Gly Thr	Ala
245		250	255
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
260		265	270
Thr Asn Ser Asp	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
275		280	285
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
290		295	300
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
305		310	315
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Gly Ala Gly Thr	Ala
320		325	330
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val
335		340	345
Thr Asn Ser Glu	Ser Ser Thr Pro Ser	Ser Gly Ala Asn Thr	Ala
350		355	360
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala
365		370	375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
380		385	390

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala	395	400	405
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	410	415	420
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala	425	430	435
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	440	445	450
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	455	460	465
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala	470	475	480
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala	485	490	495
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile	500	505	510
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe	515	520	525
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn	530	535	540
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly	545	550	555
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro	560	565	570
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile	575	580	585
Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro					590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 244

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<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
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 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
 170 175 180
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
 185 190 195
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
 200 205 210
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

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 <223> Synthetic oligonucleotide probe

<400> 249
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<400> 250
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<210> 251
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<400> 251
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<210> 252
 <211> 3781
 <212> DNA
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<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser Phe Lys Gly	Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr	Ile
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Lys Ile Leu Leu	Pro Leu Ser Gly Ser	His Leu Phe Thr Cys	Gly
140	145		150
Thr Ala Ala Phe	Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu	Asn
155	160		165
Phe Thr Leu Ala	Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu	Asp
170	175		180
Gly Lys Gly Arg	Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr	Ala
185	190		195
Leu Val Val Asp	Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser	Phe
200	205		210
Gln Gly Asn Asp	Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg	Pro
215	220		225
Thr Lys Thr Glu	Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala	Phe
230	235		240
Val Ala Ser Ala	Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln	Gly
245	250		255
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Ser Glu Thr Gly Gln	Glu
260	265		270
Phe Glu Phe Phe	Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg	Ile
275	280		285
Cys Lys Gly Asp	Glu Gly Gly Glu Arg	Val Leu Gln Gln Arg	Trp
290	295		300
Thr Ser Phe Leu	Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp	Asp
305	310		315
Gly Phe Pro Phe	Asn Val Leu Gln Asp	Val Phe Thr Leu Ser	Pro
320	325		330
Ser Pro Gln Asp	Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe	Thr
335	340		345
Ser Gln Trp His	Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys	Val
350	355		360
Phe Thr Met Lys	Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr	Lys
365	370		375
Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380	385		390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395	400		405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
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Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
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Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
				725					730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
				740					745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
				755					760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
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Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
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Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
				800					805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 258

<211> 45

<212> DNA

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Homo sapiens

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<222> 3635

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<400> 259

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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
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Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
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Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
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Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
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Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	
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Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	
				260					265					270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	

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Lys	Gly	Tyr	Ile	Arg 290	Asp	Leu	His	Asn	Ser 295	Lys	Ile	His	Gln	Ala 300
Ile	Thr	Leu	His	Pro 305	Asn	Lys	Asn	Pro	Pro 310	Tyr	Gln	Tyr	Arg	Leu 315
His	Ser	Tyr	Met	Leu 320	Ser	Arg	Lys	Ile	Ser 325	Glu	Leu	Arg	His	Arg 330
Thr	Ile	Gln	Leu	His 335	Arg	Glu	Ile	Val	Leu 340	Met	Ser	Lys	Tyr	Ser 345
Asn	Thr	Glu	Ile	His 350	Lys	Glu	Asp	Leu	Gln 355	Leu	Gly	Ile	Pro	Pro 360
Ser	Phe	Met	Arg	Phe 365	Gln	Pro	Arg	Gln	Arg 370	Glu	Glu	Ile	Leu	Glu 375
Trp	Glu	Phe	Leu	Thr 380	Gly	Lys	Tyr	Leu	Tyr 385	Ser	Ala	Val	Asp	Gly 390
Gln	Pro	Pro	Arg	Arg 395	Gly	Met	Asp	Ser	Ala 400	Gln	Arg	Glu	Ala	Leu 405
Asp	Asp	Ile	Val	Met 410	Gln	Val	Met	Glu	Met 415	Ile	Asn	Ala	Asn	Ala 420
Lys	Thr	Arg	Gly	Arg 425	Ile	Ile	Asp	Phe	Lys 430	Glu	Ile	Gln	Tyr	Gly 435
Tyr	Arg	Arg	Val	Asn 440	Pro	Met	Tyr	Gly	Ala 445	Glu	Tyr	Ile	Leu	Asp 450
Leu	Leu	Leu	Leu	Tyr 455	Lys	Lys	His	Lys	Gly 460	Lys	Lys	Met	Thr	Val 465
Pro	Val	Arg	Arg	His 470	Ala	Tyr	Leu	Gln	Gln 475	Thr	Phe	Ser	Lys	Ile 480
Gln	Phe	Val	Glu	His 485	Glu	Glu	Leu	Asp	Ala 490	Gln	Glu	Leu	Ala	Lys 495
Arg	Ile	Asn	Gln	Glu 500	Ser	Gly	Ser	Leu	Ser 505	Phe	Leu	Ser	Asn	Ser 510
Leu	Lys	Lys	Leu	Val 515	Pro	Phe	Gln	Leu	Pro 520	Gly	Ser	Lys	Ser	Glu 525
His	Lys	Glu	Pro	Lys 530	Asp	Lys	Lys	Ile	Asn 535	Ile	Leu	Ile	Pro	Leu 540
Ser	Gly	Arg	Phe	Asp 545	Met	Phe	Val	Arg	Phe 550	Met	Gly	Asn	Phe	Glu 555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu

560										565					570				
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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
				590					595					600					
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
				605					610					615					
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
				620					625					630					
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
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Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
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Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
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Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
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Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
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Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
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Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
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Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
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Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 262
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
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<210> 263
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 263
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<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

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tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
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gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccocattc 500
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 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Gln Asn Leu Val Arg
 35
 40
 45
 Ser Val Pro Ser Gln Pro Gln Arg Gln Lys Lys Ser Asn Ser
 50
 55
 60
 Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gln Ser Lys Phe Lys
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 Gln Leu Val Thr His Gly Asp Ala Ser Thr Gln Asn Asp Val Leu
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 85
 90

<210> 265
 <211> 350
 <212> PRT
 <213> Homo sapiens

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 ctgcattttt tcacagagaga aataatcata ttcttaattt caaaagtgt 1300
 aaaaattta aacctactg atattcata acaagctga ttaagcaaa 1250
 tagatcaag aggtcacag ccttataa agttattaa acaataatat 1200
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 aacaagtaaat aaattgatg acatcgaaac tgttataac atgtgtgtg 1050
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<210> 266
<211> 2403
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Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Glu 140
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Pro Ala Ala Lys Glu Thr Glu Ala Pro Arg Met Leu Pro Val Val 155
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Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro 170
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Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu 185
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Ser Glu Asp Val Pro Glu Leu Ser Gly Glu Thr Ala Ile Glu Lys 200
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Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp 215
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Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Glu Val Glu Glu Ala 230
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Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala 260
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Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Glu Leu Leu Pro 275
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Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala 335
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acattcaatc cccatttat cagcctcccc ccacagcacc ctcctacag 1350

Leu Val Gly Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala 20
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Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val 5
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<400> 267

<213> Homo sapiens

<212> PRT

<211> 466

<210> 267

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60	55	50	His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser
75	70	65	Lys Glu Met Pro Glu Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp
90	85	80	Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr
105	100	95	Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Glu Ile
120	115	110	Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly
135	130	125	Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile
150	145	140	Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Glu Pro Thr Ala
165	160	155	Lys Trp Lys Gly Pro Glu Gly Gln Asp Leu Ser Ser Asp Ser Arg
180	175	170	Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile
195	190	185	Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu
210	205	200	Ala Glu Gln Ser His Glu Val Gln Ser Lys Val Leu Ile Gly Glu
225	220	215	Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu
240	235	230	Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile
255	250	245	Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp
270	265	260	Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
285	280	275	His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
300	295	290	Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
315	310	305	Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val

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<400> 268

<213> Homo sapiens

<212> DNA

<211> 2103

<210> 268

GLY

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	Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn	380	385	390
	Gly Tyr Trp Val Leu Arg Leu Thr Thr Gln His Leu Tyr Phe Thr	395	400	405
	Phe Asn Pro His Phe Ile Ser Leu Pro Ser Thr Pro Thr	410	415	420
	Arg Val Gly Val Phe Leu Asp Tyr Gln Gly Gly Thr Ile Ser Phe	425	430	435
	Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys	440	445	450
	Gln Phe Gln Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr	455	460	465
	Asp Gln Gln Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp			

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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

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Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	

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245		250	255
Met Lys Arg Gly	Leu Arg Arg Ile Ile	Val His Glu Lys Tyr	Lys
260		265	270
His Pro Ser His	Asp Tyr Asp Ile Ser	Leu Ala Glu Leu Ser	Ser
275		280	285
Pro Val Pro Tyr	Thr Asn Ala Val His	Arg Val Cys Leu Pro	Asp
290		295	300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp	Val Met Phe Val Thr	Gly
305		310	315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr	Ser Gln Asn His Leu	Arg
320		325	330
Gln Ala Gln Val	Thr Leu Ile Asp Ala	Thr Thr Cys Asn Glu	Pro
335		340	345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro	Arg Met Leu Cys Ala	Gly
350		355	360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys	Gln Gly Asp Ser Gly	Gly
365		370	375
Pro Leu Val Ser	Ser Asp Ala Arg Asp	Ile Trp Tyr Leu Ala	Gly
380		385	390
Ile Val Ser Trp	Gly Asp Glu Cys Ala	Lys Pro Asn Lys Pro	Gly
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Val Tyr Thr Arg	Val Thr Ala Leu Arg	Asp Trp Ile Thr Ser	Lys
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Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys		50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly		65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu		80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys		95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp		110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val		125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val		140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro		155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe		170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu		185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser		200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly		215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu				230	235	

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
				125					130					135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	
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Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
				155					160					165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
				170					175					180	
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
				185					190					195	
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
				290					295					300	
Glu	Met	Glu	Glu	Leu											
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<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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<210> 275
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	

Gly Ser Leu Val	Ser Leu His Cys Leu	Ala Cys Gly Lys Ser	Leu
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Lys Thr Pro Arg	Val Val Gly Gly Glu	Glu Ala Ser Val Asp	Ser
	200	205	210
Trp Pro Trp Gln	Val Ser Ile Gln Tyr	Asp Lys Gln His Val	Cys
	215	220	225
Gly Gly Ser Ile	Leu Asp Pro His Trp	Val Leu Thr Ala Ala	His
	230	235	240
Cys Phe Arg Lys	His Thr Asp Val Phe	Asn Trp Lys Val Arg	Ala
	245	250	255
Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
	395	400	405
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<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<210> 277
 <211> 761
 <212> PRT
 <213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met Arg
200	205	210
Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu Arg
215	220	225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser Thr
230	235	240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
245	250	255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
260	265	270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr Thr
275	280	285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
290	295	300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro
305	310	315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320	325	330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335	340	345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350	355	360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365	370	375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380	385	390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395	400	405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410	415	420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425	430	435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440	445	450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455	460	465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470	475	480

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Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg
500		505	510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu
515		520	525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg
530		535	540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser
545		550	555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala
560		565	570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala
575		580	585
Leu Ala Ser Tyr	Tyr Trp Ser His Gly	Pro Ala Ala Val Pro	Glu
590		595	600
Ala Ser Ser Thr	Val Tyr Asn Gly Ser	Leu Leu Leu Ile Val	Gln
605		610	615
Asp Gly Val Gly	Gly Leu Tyr Gln Cys	Trp Ala Thr Glu Asn	Gly
620		625	630
Phe Ser Tyr Pro	Val Ile Ser Tyr Trp	Val Asp Ser Gln Asp	Gln
635		640	645
Thr Leu Ala Leu	Asp Pro Glu Leu Ala	Gly Ile Pro Arg Glu	His
650		655	660
Val Lys Val Pro	Leu Thr Arg Val Ser	Gly Gly Ala Ala Leu	Ala
665		670	675
Ala Gln Gln Ser	Tyr Trp Pro His Phe	Val Thr Val Thr Val	Leu
680		685	690
Phe Ala Leu Val	Leu Ser Gly Ala Leu	Ile Ile Leu Val Ala	Ser
695		700	705
Pro Leu Arg Ala	Leu Arg Ala Arg Gly	Lys Val Gln Gly Cys	Glu
710		715	720
Thr Leu Arg Pro	Gly Glu Lys Ala Pro	Leu Ser Arg Glu Gln	His
725		730	735
Leu Gln Ser Pro	Lys Glu Cys Arg Thr	Ser Ala Ser Asp Val	Asp
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Ala Asp Asn Asn	Cys Leu Gly Thr Glu	Val Ala	
755		760	

<210> 278
<211> 24
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgatca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

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 gtccctgtct ctggtgccc aagttagctc cttcttggt gagcaggcat 2250
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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
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 20 25 30
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155										160					165				
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro					
				170					175					180					
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met					
				185					190					195					
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe					
				200					205					210					
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile					
				215					220					225					
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu					
				230					235					240					
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe					
				245					250					255					
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly					
				260					265					270					
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn					
				275					280					285					
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu					
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Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu					
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Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys					
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Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn					
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Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His					
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Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile					
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Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu					
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Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys					
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Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu					
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Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser					
				425					430					435					
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser					

440	445	450
Pro Thr Gln Arg	Leu Val Gly Trp Ile Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr	His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr	Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala	
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Val Trp Trp Leu	Arg Gly Ala Arg Lys Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 283
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<210> 284
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 285
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<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
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 ccacctctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
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 caactagaga atggtgggtca gtgagacact atagaattac taaggagaag 2250
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
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<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagagggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

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<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292
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 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

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ccgacgcagg gccggggccg gccaggggcc gaggagcgcg gcggccagag 100

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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
				350					355					360					
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
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<210> 299
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
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<210> 300
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<210> 301
 <211> 1334
 <212> DNA
 <213> Homo sapiens

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 acagagtga actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	65		70		75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr					
	80		85		90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln					
	95		100		105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu					
	110		115		120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr					
	125		130		135
Cys Gly Val Leu Leu Ser Phe Leu					
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<210> 303

<211> 1768

<212> DNA

<213> Homo sapiens

<400> 303

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<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

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				20					25					30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
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	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
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Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
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Arg Arg Arg Asp					

<210> 305
 <211> 989
 <212> DNA
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<210> 306
<211> 262
<212> PRT
<213> Homo sapiens

<400> 306

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Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser	
				50					55					60	
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
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Leu Thr Leu Ala Phe Lys Ile
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<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

35										40					45				
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro					
				50					55					60					
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys					
				65					70					75					
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala					
				80					85					90					
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala					
				95					100					105					
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp					
				110					115					120					
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala					
				125					130					135					
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser					
				140					145					150					
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
				260					265					270					
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
				275					280					285					
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
				305					310					315					
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg					

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Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Arg	Leu	Arg	Glu	Gln				
				335										340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly					
				350										355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg					
				365										370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly					
				380										385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu					
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Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser					
				410										415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg					
				425										430					435
Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr					
				440										445					450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys					
				455										460					465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser					
				470										475					480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg					
				485										490					495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser					
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Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys					
				515										520					525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala					
				530										535					540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile					
				545										550					555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys					
				560										565					570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala					
				575										580					585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala					
				590										595					600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu					

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Cys Gly Ser Ser	Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro			
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Asp Leu Asp Arg	Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg Ala			
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 <213> Homo sapiens

<400> 309
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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	His	Leu	Phe	Pro	Ala	Leu	Met	Met	Leu	Ser	Met	Thr	Met	Leu
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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
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Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
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Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
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Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile
				80					85					90

Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
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Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120

Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135

Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150

Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165

Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180

Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195

Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210

Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
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His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly

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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu
				260					265					270
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
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Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
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Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
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Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335					340					345
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
				350					355					360
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His
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Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile
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Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro
				395					400					405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe
				410					415					420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala
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Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr
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Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp
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Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val
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Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu
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Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu
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Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly

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Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser
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Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr
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Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu
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Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu
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Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu
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Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp
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His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp
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Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 312

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

gcttggacat gtaccaggcc gtgg 24

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

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 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 315
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 35 40 45
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150

Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
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Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
				170					175					180	
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
				185					190					195	
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
				200					205					210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
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Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
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Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	
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<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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			20						25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
			35						40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
			140						145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
			155						160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
			170						175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
			185						190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
			200						205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
			215						220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
			230						235					240

Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245										250					255				
Pro	Ser	Ile	Arg	Asn	Pro	Val	Ser	Leu	Val	Val	Thr	Arg	Leu	Val					
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Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	Gly	Pro	Ser	Ala					
				275					280					285					
Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn					
				290					295					300					
Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu					
				305					310					315					
Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu					
				320					325					330					
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys					
				335					340					345					
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala					
				350					355					360					
His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys					
				365					370					375					
Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val					
				380					385					390					
Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser					
				395					400					405					
Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr					
				410					415					420					
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro					
				425					430					435					
Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln					
				440					445					450					
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro					
				455					460					465					
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala					
				470					475					480					
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys					
				485					490					495					
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp					
				500					505					510					
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro					
				515					520					525					
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val					

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Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly					
				545					550					555					
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn					
				560					565					570					
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu					
				575					580					585					
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe					
				590					595					600					
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro					
				605					610					615					
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr					
				620					625					630					
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser					
				635					640					645					
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala					
				650					655					660					
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys					
				665					670					675					
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly					
				680					685					690					
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile					
				695					700					705					
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro					
				710					715					720					
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser					
				725					730					735					
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp					
				740					745					750					
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr					
				755					760					765					
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro					
				770					775					780					
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg					
				785					790					795					
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro					
				800					805					810					
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu					

815

820

825

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<210> 318

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

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<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctgtgctctt cggatgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgtttggta tcttggccct aactctaatt gtcctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aatatctcag aagcggaaat ggactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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<210> 322
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322
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 Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
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 Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
 35 40 45
 Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
 50 55 60
 Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
 65 70 75
 Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe

80					85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe
				95					100					105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys
				110					115					120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro
				125					130					135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe
				140					145					150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn
				155					160					165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn
				170					175					180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala
				200					205					210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro
				215					220					225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu
				230					235					240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe
				245					250					255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg
				260					265					270
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly
				275					280					285
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys
				290					295					300
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly
				305					310					315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgactggc ggaggacagc gcacgtgggc 200
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

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	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 200

aaccccggtca cctccgtggt ccagtagcaa gggctctgga ggagctgcgt 250
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 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagtgcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
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<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
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 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly
 80 85 90
 Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg
 95 100 105
 Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr
 110 115 120
 Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly
 125 130 135
 Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser
 140 145 150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val	
				155					160					165	
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val	
				170					175					180	
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala	
				185					190					195	
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser	
				200					205					210	
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe	
				215					220					225	
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile	
				230					235					240	
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro	
				245					250					255	
Ser	Lys	His	Asp	Tyr	Val										
				260											

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
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 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350
 tgctgcttcc gtgatgtcct tcttggttt catgatggcc atccttgga 400
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 ttttctaatt 2010

<211> 225
<212> PRT
<213> Homo sapiens

<400> 328

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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp
				20					25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
				35					40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
				50					55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
				80					85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
				110					115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
				125					130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
				140					145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
				155					160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
				170					175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
				185					190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
				200					205					210
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
<211> 1315
<212> DNA
<213> Homo sapiens

<400> 329

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 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
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 ttgctggggc caagtgtacc acctgtgtg aggagaagga ttccaaggcc 350
 cgctgtgtg tcacctctg gattgtctt gtcatctcag ggtcctgac 400
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 ctgcacttg ccctcggggg ggtcccagg cccagccat tacatggccc 600
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 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250
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 tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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 gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggg 200
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
 ggaagggctc tggatgaatt gcatccgaca agccaggggc cggttgcaat 300
 gcaagttcta tagctccttg ttggctctcc cgctgcctt ggaaacagcc 350
 cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
 tggcatctgt ggcatagaag aggtccagtg cacaggctct aacgagaggg 450
 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
 atcttcgttc tgattccggg gagctggaca gccaatataa tcatcagaga 550
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 cacttttctt tggctgggca agcgctgctg tcctcttcat tggagggggg 650
 ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700
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 ccaagtatgg actatgggtc atgtttttta taaagtcttg ctagaaactg 850
 taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
 cgaaagtttc aatttggtac tgggtggtagg aatgaaaatg acttacttgg 950
 acattctgac ttcaggtgta ttaaatgcat tgactattgt tggaccaat 1000
 cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
 caagtgtaca atgatggact acttattact ttttgacat catgtattat 1100
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
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Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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ctcagaagct gctagtctgt ctcaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
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tttttaacac gtcaataaaa aaataatctc ccaga 535

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<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334
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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75
Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335
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ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200
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gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
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cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
1				5					10					15

Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
				20					25					30

Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
				35					40					45

Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
				50					55					60

Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65					70					75

Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80					85					90

Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95					100					105

Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110					115					120

Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125					130					135

Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr
				140					145			

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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 aaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
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 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccagggtg ctgcagctgg 250

aggacttgga tgggtttgag gggttactccc tgagtgactg gctgtgcctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gtccggagca cgggggatga acaactgggt agaatggagg ttgcaactgt 550
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
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 ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccgggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caaccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttggcaa 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
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aagccagcaa gcacagccct gaagccaggc accgcctgga ctttggggaa 650
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gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
tctgtttcca tgatgaggcc tggccactc tctgctggac tgtacacagc 1100
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cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200
ccaggctgga ggggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250

atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300
 cttcatggat gccactgcg agtgccaccc aggtggctg gagcccctcc 1350
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 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
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 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850
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<210> 347

<211> 639

<212> PRT
<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala	His
	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg	Ile
	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val	Ile
	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln	Arg
	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu	Pro
	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile	Arg
	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His	Tyr
	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg	Gly
	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly	Gly
	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr	Gln
	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu	Arg
	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys	Glu
	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys	Ala
	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg	Leu
	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro	Glu
	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu	His
	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly	Asp
	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser	Arg
	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His	Phe
	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val
				560					565					570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln
				575					580					585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser
				590					595					600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu
				605					610					615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe
				620					625					630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg						
				635										

<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgtg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens

<400> 351

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ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtgc 200
caggggagggc ccctcggccc cacgtcatgt gtgctgtgtg gagcgagcac 250
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cctggcactg cccccccagc cccccatca ggctttgagg aggggccgcc 350
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tttgagccc ctcatgggct cgcaaccca caccctaact cagactccat 500
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120
 Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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 gttggccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550
agtagcccc agaggcgctg ggagtgttg caccgccctc cctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctcggggc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccatctctg caacaactgc acagactcgc 750
acgtcgctg ctttggctat aactgcgagt agggctcagg catcacacc 800
accggtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
gggtccccg ccttcacct ggctgtcatc gggtagggcg gggcgtggg 900
ttcagggcg caccacttc aagcctgtgt cccacaggtc ctggcgag 950
tggaagtcag ctgtccagg cctcctgaac tacataaata actggcaca 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcccacgtc 1100
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgaggag 1150
gcggctgcag tccttttctc cctcaaagg ctccgacct cagctggagg 1200
cgggcatctt tcctaaagg tcccatagg gtctggttcc acccatccc 1250
aggtctgtgg tcagagcctg ggagggttcc ctacgatggt taggggtgcc 1300
ccatggagg gctgactgcc ccacattgcc ttccagacag gacacgagca 1350
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400
agaggaggg ggctagggg tcctctagat cagtggggc actgcaggtg 1450
gggctctccc tatacctgg acacctgctg gatgtcacct ctgcaaccac 1500

acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550
 cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
 cataggacca cacgtcccag ctgggaggag aggcctgggg ccccaggga 1750
 gggaggcagg ggggtgggga catggagagc tgaggcagcc tcgtctcccc 1800
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
 gctgggcctg ccccaggga acgtgggggc ggagactcag ctggacagcc 1950
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg acccctctc 2000
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1 5 10 15
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln

	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150
Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357
 <211> 1536
 <212> DNA
 <213> Homo sapiens

<400> 357
 agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50
 cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
 ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150
 acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
 cataggcttc ttccaggatt tagaaatacc agcagtgccc atactccata 250
 gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
 gaggtttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
 cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
 tcagattcat ctctcctga taatgaacaa ggcctccca gagtatgaag 550
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
 ctctttattc tgggtggacag tggatatgaaa gaaaatggga aggtgatatc 650
 atttttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
 ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
 catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
 ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
 aactcaaate tcagagacac taaacaacag gatcactagg cctgccaacc 950
 acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
 gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
 tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200
 ctagagaaaag attgttccaa ttgttcattt aatatcaagt ttgtatactg 1250
 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
 tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400
 cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35					40					45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 359
 ccagcagtgcc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccca ggcgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgtggc tgtggtcggt gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgctttctgg atctcaccag ggcccagtcata tatatgcaca gttagaccac 900
tccggcgac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
 ccttttaatc taagggtta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattggg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggctcact tcattctgga cacagttgga 1700
 tcaataactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
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Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	
				95					100					105	
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	
				110					115					120	
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	
				125					130					135	
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	
				140					145					150	
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	
				155					160					165	
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	
				170					175					180	
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	
				185					190					195	
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	
				200					205					210	
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	
				215					220					225	
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	
				230					235					240	
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	
				245					250					255	
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		
				260					265						

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50

cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100

ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150

tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200

aggggcgcgg ccccggcgca gtccccgcg gcccccgacc ctgaggcgtc 250

gcctctggcc gagccgccac aggagcagtc cctcgccccg tgggtctccgc 300

agacccccgc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350

agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcat 400

agtgggttga gtttctgtag atggaaaaga agtctggtca gaaggttttag 450
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500
 cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaaggtttc tgtcacaaca 650
 agattactga tttcccattht aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
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 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggt aatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactattht tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg Gly Ala Ala	Pro Ala Gln Ser Pro	Ala Ala Pro Asp Pro	Glu
	65	70	75
Ala Ser Pro Leu	Ala Glu Pro Pro Gln	Glu Gln Ser Leu Ala	Pro
	80	85	90
Trp Ser Pro Gln	Thr Pro Ala Pro Pro	Cys Ser Arg Cys Phe	Ala
	95	100	105
Arg Ala Ile Glu	Ser Ser Arg Asp Leu	Leu His Arg Ile Lys	Asp
	110	115	120
Glu Val Gly Ala	Pro Gly Ile Val Val	Gly Val Ser Val Asp	Gly
	125	130	135
Lys Glu Val Trp	Ser Glu Gly Leu Gly	Tyr Ala Asp Val Glu	Asn
	140	145	150
Arg Val Pro Cys	Lys Pro Glu Thr Val	Met Arg Ile Ala Ser	Ile
	155	160	165
Ser Lys Ser Leu	Thr Met Val Ala Leu	Ala Lys Leu Trp Glu	Ala
	170	175	180
Gly Lys Leu Asp	Leu Asp Ile Pro Val	Gln His Tyr Val Pro	Glu
	185	190	195
Phe Pro Glu Lys	Glu Tyr Glu Gly Glu	Lys Val Ser Val Thr	Thr
	200	205	210
Arg Leu Leu Ile	Ser His Leu Ser Gly	Ile Arg His Tyr Glu	Lys
	215	220	225
Asp Ile Lys Lys	Val Lys Glu Glu Lys	Ala Tyr Lys Ala Leu	Lys
	230	235	240
Met Met Lys Glu	Asn Val Ala Phe Glu	Gln Glu Lys Glu Gly	Lys
	245	250	255
Ser Asn Glu Lys	Asn Asp Phe Thr Lys	Phe Lys Thr Glu Gln	Glu
	260	265	270
Asn Glu Ala Lys	Cys Arg Asn Ser Lys	Pro Gly Lys Lys Lys	Asn
	275	280	285
Asp Phe Glu Gln	Gly Glu Leu Tyr Leu	Arg Glu Lys Phe Glu	Asn
	290	295	300
Ser Ile Glu Ser	Leu Arg Leu Phe Lys	Asn Asp Pro Leu Phe	Phe
	305	310	315
Lys Pro Gly Ser	Gln Phe Leu Tyr Ser	Thr Phe Gly Tyr Thr	Leu
	320	325	330
Leu Ala Ala Ile	Val Glu Arg Ala Ser	Gly Cys Lys Tyr Leu	Asp
	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagagaa gtctggtcag aaggttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttgctt cattctcctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggg agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccggggc gggactgggt cgcgaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
 tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcgga 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctggtg gctatgtctc ctcccttgtc cctgcgtgct ccctggtgga 500
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
 gccaccaca gcccaggcc ctgagacggc ggcccttcatt gagcgccctg 700
 agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750
 ttgcgcaaact actggatgta catcattccc gtcgtcctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggctcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200
ctaaaccccc tgggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggacttct atcaggctcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctcttctcc ctgacttact cactatgctg cttaaccaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggcttggtat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgccgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgccctga gctgtaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtgggttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650
 ctctgtgtta ctcccattta gaaaataaac acttttaa at gatcaaaaaa 1700
 aaaaaa 1706

<210> 374
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	20	25	30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	35	40	45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	50	55	60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	65	70	75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	80	85	90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	95	100	105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	110	115	120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	125	130	135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	140	145	150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	155	160	165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	170	175	180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	185	190	195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	200	205	210	

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	215	220	225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	230	235	240
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcgg ccacacggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatctttcac acaaggatg agcagattca 250
 ccttgcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
 gacggctaca tgatccgcg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcgtt gctaggctga aaggaagcc acaccactgg ccttcccttc 800
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10					15	
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25					30	
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377
 <211> 496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tgggtcaagca agtgactggg aaaatgcca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15

Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
				20					25					30

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
				35					40					45

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
				50					55					60

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
				65					70					75

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
				80					85					90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
				95					100					105

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
				110					115	

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50
ggcgatgtgg aggggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgtgtgt cacgcttgcc 150
ctcctggggg gccccacctg ggcaggggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
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tttggaagc ttgatggcca gatctcctct gcctaccca gccaagaggg 500
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggtatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	
				20					25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	
				35					40					45	
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	
				50					55					60	
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	
				65					70					75	
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	
				80					85					90	
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	
				95					100					105	
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	
				110					115					120	
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	
				125					130					135	
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	
				140					145					150	
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	
				155					160					165	
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			
				170					175						

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150

atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200

cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300

tggtgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttccaaa atcgggtccat ctcccaaggg gtccaatttt tcttcctggg 400

tgtcagcgag ccctgactca ctacagtga gctgacagg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
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aacctggaac ttttgacct gggatataac cggatccgaa gtttagccag 1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
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cagaaccttt acttgcatg gaataaaatc agtgatcatag gacagaccat 1250
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ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900

aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
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 ttgtataaga ccctttactg attccattaa tgcgcattt gttttaagat 2350
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<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala
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Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
				20					25					30
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
				35					40					45
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
				50					55					60
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
				65					70					75
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
				80					85					90
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
				95					100					105
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
				110					115					120
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
				125					130					135
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
				140					145					150

Glu Gln Phe Arg Gly Leu Arg Lys Leu	Leu Ser Leu His Leu Arg	155	160	165
Ser Asn Ser Leu Arg Thr Ile Pro Val	Arg Ile Phe Gln Asp Cys	170	175	180
Arg Asn Leu Glu Leu Leu Asp Leu Gly	Tyr Asn Arg Ile Arg Ser	185	190	195
Leu Ala Arg Asn Val Phe Ala Gly Met	Ile Arg Leu Lys Glu Leu	200	205	210
His Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys	230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu	245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly	260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu	275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser	290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu	305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe	320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu	335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile	350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu	365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu	380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly	395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile	410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu	425	430	435

Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440					445					450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455					460					465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470					475					480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485					490					495
Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
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gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200
aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250
gcagctcttc tctgtggagc tgtggctcctc tgcctccagt gctggctgag 300
gagacccga attgattctc acaggcgcac catggcagtt tttgctgttg 350
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatcctg ttctgctcc 450
atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
tctgctttaa actctttcct agcatggggc ccataaaaat tattataatt 900
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
ccaacacggg gagaaaagaa aatttccct tttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtgc gcattttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390
<211> 146
<212> PRT
<213> Homo sapiens

<400> 390
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
1 5 10 15
Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu
50 55 60
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
cttttcagtg tcacctcagc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaagtc agatgccct tttaaactcc 250
ctcttcaaaa ctcatctct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttggt gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaata actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtgga tgctcgagaac ggtgcttcta 650
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attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ccttggtgtg ctccatccac tgtggattat atcctatggc 900
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acctttatgt gaagaaatta attatatgcc attgccaggT 2340

<211> 140
<212> PRT
<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	
Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20				25					30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35				40					45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50				55					60	
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65				70					75	
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80				85					90	
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95				100					105	
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110				115					120	
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125				130					135	
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 396

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accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
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gggcccgggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
caccagcatc tcacccactg ctttctcccg ctttcgctac ctggagtcgc 400

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cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30

Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45

Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60

Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75

Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe	Ser
95	100		105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly	Leu
110	115		120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser	Asp
125	130		135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser	Ala
140	145		150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu	Ser
155	160		165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
170	175		180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
185	190		195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
200	205		210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
215	220		225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
230	235		240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
245	250		255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
260	265		270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
275	280		285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
290	295		300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
305	310		315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
320	325		330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
335	340		345
Ala Ala Arg Gly	Pro Thr Ile Leu		
350			

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600
 tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatatttaa 650
 aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700
 ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750
 atgacatgcc attgtgggga ggaagcaatg aagaaatata gccagattct 800
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 gggaaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcacgac ccaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100
 atttttgtaa tatctttctg ctattggata tatttattag ttaatatatt 1150
 tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaatctt agaagagtgg 1300
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	

Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25					30

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40					45

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	
				50					55					60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	
				65					70					75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	
				80					85					90	
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	
				95					100					105	
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	
				110					115					120	
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	
				125					130					135	
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	
				140					145					150	
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	
				155					160					165	
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	
				170					175					180	
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	
				185					190					195	
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	
				200					205					210	
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	
				215					220					225	
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	
				230					235					240	
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	
				245					250					255	
Trp	Met	Glu	Glu	Thr	Glu										
				260											

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
cacccgccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggagggat gatggctggg gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650
accacttatg atacagtga aactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgacct cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
1				5					10					15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr		
	260	270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly		
	275	285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met		
	290	300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg		
	305	315
Glu Met Ser Gly Val Ser Pro Phe		
	320	

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cgagcgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttgcca gaatgtgaat gtattgactg gaggtagaga 200

agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcattg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
 ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550
 tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag gggtacatca 900
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 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaacccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgcaat gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaagggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 413

atggcaggct tcctagataa ttttcgttg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

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gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcct ggccctcacc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaaggtgct 1100
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200

accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	1	5	10	15
Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
attctctcca cagacagctg gttc 24

<210> 421

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
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tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcttccctcc 200
ctctctctct gcctgtccta gtctcttagt cctcaaattc ccagtcacct 250
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acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
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ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtc 850
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggtg 1050
 cagaactacc gagcccttca gcctctcaat cagcgcacatgg tctttgcttc 1100
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc 1200
 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
 catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
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 cttccccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
 gaaatcgctg tgttggttaat gcagaganca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
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<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

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Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln	20	25	30	
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln	35	40	45	
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp	50	55	60	
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu	65	70	75	
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu	80	85	90	

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100 105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly
110	115 120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr	Phe Ala Glu Leu His
125	130 135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp	Ser Leu Ser Glu Ala
140	145 150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu	Gly Ile Leu Ile Glu
155	160 165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu	His Ile Leu Ser His
170	175 180
Leu His Glu Val Arg His Lys Asp Gln Lys	Thr Ser Val Pro Pro
185	190 195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln	Leu Gly Gln Tyr Phe
200	205 210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro	Cys Tyr Gln Ser Val
215	220 225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln	Ile Ser Met Glu Gln
230	235 240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser	Thr Glu Glu Glu Pro
245	250 255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala	Leu Gln Pro Leu Asn
260	265 270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln	Ala Gly Ser Ser Tyr
275	280 285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val	Gly Ile Leu Val Gly
290	295 300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe	Ile Ala Arg Lys Ile
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<220>
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<210> 425
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<212> DNA
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<220>
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<400> 425
cccgatctgc ctgctgta 18

<210> 426
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<212> DNA
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<220>
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<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
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<213> Artificial Sequence

<220>
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<400> 427
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<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

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gattctactg tTTTgtcttc taggatcaac tCGgtcatta ccacagctca 150
aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350
 ggggtgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatacctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccacccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
 agcaaattgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
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 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30

Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45

Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50					55					60

Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65					70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90

Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
	110	115	120
Gln Ile Phe Thr	Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly		
	125	130	135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp		
	140	145	150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln		
	155	160	165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp		
	170	175	180
Asp Phe Ala Val	Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His		
	185	190	195
Ala Ile Glu Glu	Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln		
	200	205	

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgccctt gagatcccca aggggaagca 250
aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt taaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgct 600
agcgttggtt tttcacattc aatggagctg aatgttcagg acctcttccc 650
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aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
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tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
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<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

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Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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<213> Artificial Sequence

<220>

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<210> 434

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<400> 434

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<210> 435
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<220>
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cccacctgta ccacatgt 19

<210> 436
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actccaggca ccatctgttc tccc 24

<210> 437
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aagggctggc attcaagtc 19

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tgacctggca aaggaagaa 19

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cagccaccct ccagtccaag g 21

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gggtcgtggtt ttggagaga 19

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tcctccatca cttcccctag ctcca 25

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<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
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aaaggacacc gggatgtg 18

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<210> 471
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<210> 474

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<213> Artificial Sequence

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